



SEQUENCE LISTING

<110> TOYO BOSEKI KABUSHIKI KAISHA
<120> MODIFIED THERMOSTABLE DNA POLYMERASE
<130> 10089/14
<140> US 09/852,922
<141> 2001-05-10
<150> JP 2000-138796
<151> 2000-05-11
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cctggattgt tctacaagat tatgggggat gaaag atg atc ctc gac act gac 173
Met Ile Leu Asp Thr Asp
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tac ata acc gag gat gga aag cct gtc ata aga att ttc aag aag gaa 221
Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile Arg Ile Phe Lys Lys Glu
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aac ggc gag ttt aag att gag tac gac cgg act ttt gaa ccc tac ttc 269
Asn Gly Glu Phe Lys Ile Glu Tyr Asp Arg Thr Phe Glu Pro Tyr Phe
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Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile Glu Glu Val Lys Lys Ile
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acc gcc gag agg cac ggg acg gtt gta acg gtt aag cgg gtt gaa aag 365
Thr Ala Glu Arg His Gly Thr Val Val Thr Val Lys Arg Val Glu Lys
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Val Gln Lys Lys Phe Leu Gly Arg Pro Val Glu Val Trp Lys Leu Tyr
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Phe Thr His Pro Gln Asp Val Pro Ala Ile Arg Asp Lys Ile Arg Glu
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His Gly Ala Val Ile Asp Ile Tyr Glu Tyr Asp Ile Pro Phe Ala Lys
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cgc tac ctc ata gac aag gga tta gtg cca atg gaa ggc gac gag gag 557

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Lys	Glu	Lys	Asp	Pro	Asp	Val	Leu	Ile	Thr	Tyr	Asn	Gly	Asp	Asn	Phe		
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Lys Glu Leu Ala Arg Arg Gln Ser Tyr Glu Gly Gly Tyr Val Lys			
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gag ccc gag aga ggg ttg tgg gag aac ata gtg tac cta gat ttt aga	1373		
Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile Val Tyr Leu Asp Phe Arg			
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tgc cat cca gcc gat acg aag gtt gtc gtc aag ggg aag ggg att ata	1421		
Cys His Pro Ala Asp Thr Lys Val Val Val Lys Gly Lys Gly Ile Ile			
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Asn Ile Ser Glu Val Gln Glu Gly Asp Tyr Val Leu Gly Ile Asp Gly			
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Trp Gln Arg Val Arg Lys Val Trp Glu Tyr Asp Tyr Lys Gly Glu Leu			
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gta aac ata aac ggg tta aag tgt acg ccc aat cat aag ctt ccc gtt	1565		
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Val Thr Lys Asn Glu Arg Gln Thr Arg Ile Arg Asp Ser Leu Ala Lys			
475	480	485	
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Ser Phe Leu Thr Lys Lys Val Lys Gly Lys Ile Ile Thr Thr Pro Leu			
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Phe Tyr Glu Ile Gly Arg Ala Thr Ser Glu Asn Ile Pro Glu Glu Glu			
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Val Leu Lys Gly Glu Leu Ala Gly Ile Leu Leu Ala Glu Gly Thr Leu			
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Ile Ser His Gln Tyr Arg Val Glu Ile Thr Ile Gly Lys Asp Glu Glu			
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Val Ala Lys Lys Asn Val Tyr Leu Lys Val Lys Glu Ile Met Asp Asn	
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615 620 625 630	
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Asp Gly Ser Val Asn Arg Val Arg Arg Ser Ile Val Ala Thr Gln Gly	
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ctt ggt atc cct cat caa acg tac acg tat cag tat cag gaa aat ggg	2189
Leu Gly Ile Pro His Gln Thr Tyr Thr Tyr Gln Tyr Gln Glu Asn Gly	
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Ile Leu Phe Gln Thr Leu Ile Gly Phe Ile Ser Glu Arg Lys Asn Ala	
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Asn Gly Phe Tyr Arg Leu Ser Glu Phe Asn Val Ser Thr Glu Tyr Tyr	
730 735 740	
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Glu Gly Lys Val Tyr Asp Leu Thr Leu Glu Gly Thr Pro Tyr Tyr Phe	
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Ala Asn Gly Ile Leu Thr His Asn Ser Leu Tyr Pro Ser Ile Ile Ile	
760 765 770	
acc cac aac gtc tcg ccg gat acg ctc aac aga gaa gga tgc aag gaa	2525
Thr His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Lys Glu	
775 780 785 790	
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Tyr Asp Val Ala Pro Gln Val Gly His Arg Phe Cys Lys Asp Phe Pro	
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Gly Phe Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys	
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Ile Lys Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Arg Lys Leu	
825 830 835	
ctc gat tac agg cag agg gcc atc aag atc ctg gca aac agc atc cta	2717
Leu Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Ile Leu	
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855 860 865 870	
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Arg Ile Gly Glu Leu Ile Asp Arg Met Met Glu Glu Asn Ala Gly Lys	
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Val Lys Arg Glu Gly Glu Thr Glu Val Leu Glu Val Ser Gly Leu Glu	
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Val Pro Ser Phe Asn Arg Arg Thr Asn Lys Ala Glu Leu Lys Arg Val	
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Ser Val Arg Asn Gly Glu Leu Val Glu Val Thr Gly Asp Glu Leu Lys	
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Pro Gly Asp Leu Val Ala Val Pro Arg Arg Leu Glu Leu Pro Glu Arg	
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Asn His Val Leu Asn Leu Val Glu Leu Leu Leu Gly Thr Pro Glu Glu	
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gaa act ttg gac atc gtc atg acg atc cca gtc aag ggt aag aag aac	3197
Glu Thr Leu Asp Ile Val Met Thr Ile Pro Val Lys Gly Lys Lys Asn	
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Phe Phe Lys Gly Met Leu Arg Thr Leu Arg Trp Ile Phe Gly Glu Glu	
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Lys Arg Pro Arg Thr Ala Arg Arg Tyr Leu Arg His Leu Glu Asp Leu	
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Gly Tyr Val Arg Leu Lys Lys Ile Gly Tyr Glu Val Leu Asp Trp Asp	
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tca ctt aag aac tac aga agg ctc tac gag gcg ctt gtc gag aac gtc	3389
Ser Leu Lys Asn Tyr Arg Arg Leu Tyr Glu Ala Leu Val Glu Asn Val	
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Arg Tyr Asn Gly Asn Lys Arg Glu Tyr Leu Val Glu Phe Asn Ser Ile	
1080 1085 1090	
cgg gat gca gtt ggc ata atg ccc cta aaa gag ctg aag gag tgg aag	3485
Arg Asp Ala Val Gly Ile Met Pro Leu Lys Glu Leu Lys Glu Trp Lys	
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Ile Gly Thr Leu Asn Gly Phe Arg Met Arg Lys Leu Ile Glu Val Asp	
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Val Lys Leu Asp Lys Lys Lys Asn Ala Tyr Tyr Ser His Val Ile Pro				
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Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys Lys Tyr Ala Val Ile Asp				
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<212> PRT

<213> *Pyrococcus kodakaraensis*

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Ser	Tyr	Ala	Asp	Glu	Glu	Gly	Ala	Arg	Val	Ile	Thr	Trp	Lys	Asn	Val	
				165					170					175		
Asp	Leu	Pro	Tyr	Val	Asp	Val	Val	Ser	Thr	Glu	Arg	Glu	Met	Ile	Lys	
			180					185					190			
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		195					200					205				
Tyr	Asn	Gly	Asp	Asn	Phe	Asp	Phe	Ala	Tyr	Leu	Lys	Lys	Arg	Cys	Glu	
	210					215					220					
Lys	Leu	Gly	Ile	Asn	Phe	Ala	Leu	Gly	Arg	Asp	Gly	Ser	Glu	Pro	Lys	
225					230					235					240	
Ile	Gln	Arg	Met	Gly	Asp	Arg	Phe	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	
				245					250					255		
His	Phe	Asp	Leu	Tyr	Pro	Val	Ile	Arg	Arg	Thr	Ile	Asn	Leu	Pro	Thr	
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Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Val	Phe	Gly	Gln	Pro	Lys	Glu	
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Lys	Val	Tyr	Ala	Glu	Glu	Ile	Thr	Thr	Ala	Trp	Glu	Thr	Gly	Glu	Asn	
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Leu	Glu	Arg	Val	Ala	Arg	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Val	Thr	Tyr	
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Glu	Leu	Gly	Lys	Glu	Phe	Leu	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu	
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Ile	Gly	Gln	Ser	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	
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Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala	
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Pro	Asn	Lys	Pro	Asp	Glu	Lys	Glu	Leu	Ala	Arg	Arg	Arg	Gln	Ser	Tyr	
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Glu	Gly	Gly	Tyr	Val	Lys	Glu	Pro	Glu	Arg	Gly	Leu	Trp	Glu	Asn	Ile	
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Val	Tyr	Leu	Asp	Phe	Arg	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	His	
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Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Lys	Glu	Tyr	Asp	
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Val	Ala	Pro	Gln	Val	Gly	His	Arg	Phe	Cys	Lys	Asp	Phe	Pro	Gly	Phe	
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Tyr	Gly	Tyr	Ala	Arg	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Cys	Ala	Glu	Ser	
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 Arg Val Leu Glu Ala Leu Leu Lys Asp Gly Asp Val Glu Lys Ala Val
 625 630 635 640
 Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
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 Pro Glu Lys Leu Val Ile His Glu Gln Ile Thr Arg Asp Leu Lys Asp
 660 665 670
 Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala
 675 680 685
 Arg Gly Val Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
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 Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
 705 710 715 720
 Asp Pro Thr Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln
 725 730 735
 Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
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 <213> *Pyrococcus kodakaraensis*

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 ctctgaagg acgattctgc cattgaggaa gtcaagaaga taaccgccga gaggcacggg 180
 acggttgtaa cggttaagcg ggttgaaaag gttcagaaga agttcctcgg gagaccagtt 240
 gaggtctgga aactctactt tactcatccg caggacgtcc cagcgataag ggacaagata 300
 cgagagcatc cagcagttat tgacatctac gagtacgaca tacccttcgc caagcgctac 360
 ctcatagaca agggattagt gccaatggaa ggcgacgagg agctgaaaat gctcgccctt 420
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 accggcgaga accttgagag agtcgccccg tactcgatgg aagatgcgaa gggtcacatac 960

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<211> 34

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<213> Artificial Sequence

<220>

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34

<210> 5

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<210> 6

<211> 34

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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<220>
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 <210> 12
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 <210> 13
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 <212> DNA
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 <223> Description of Artificial Sequence:primer

 <400> 13
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 <210> 14
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 <210> 15
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 <210> 16
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<212> DNA
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 <210> 17
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 <400> 17
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 <210> 18
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 <220>
 <223> Description of Artificial Sequence:primer

 <400> 18
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 <210> 19
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 <220>
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 <210> 20
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 <220>
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 <223> Description of Artificial Sequence:primer

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 <210> 25
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 <212> DNA
 <213> Artificial Sequence

 <220>
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<400> 25
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<210> 26
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<212> DNA
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<220>
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<210> 27
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<212> DNA
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<220>
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<220>
<223> Description of Artificial Sequence:primer

<400> 28
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<210> 29
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<213> Pyrococcus

<400> 29

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1 5 10

<210> 30
<211> 13
<212> PRT
<213> Pyrococcus

<400> 30

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1 5 10

<210> 31
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<213> Thermococcus

<400> 31

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1 5 10

<210> 32
<211> 13
<212> PRT
<213> Sulfolobus

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1 5 10

<210> 33
<211> 13
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<213> T7 phage

<400> 33

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<210> 34
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<400> 34

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1 5 10

<210> 35
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<212> PRT
<213> Pyrococcus or Thermococcus

<400> 35

Asp Ile Glu Thr Lys Tyr His
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<210> 36
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<212> PRT
<213> Pyrococcus or Thermococcus

<400> 36

Asp Ile Glu Thr Phe Tyr His
1 5

<210> 37
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<212> PRT
<213> Pyrococcus or Thermococcus

<400> 37

Asp Ile Glu Thr Lys Tyr
1 5